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P14922;
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"Developmental biochemistry of cottonseed embryogenesis
germination. XIX. Sequences and genomic organization of
globulin (vicilin) genes of cottonseed.";
plant Mol. Biol. 9:533-546(1987).
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01-APR-1990 (Rel. 14, Last seg
01-FEB-1995 (Rel. 31, Last ann
repression in yeast.";
Gene 73:97-111(1988).
                                                 MEDLINE=89211964;
                                                             SEQUENCE FROM
                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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                                      Trumbly R.J.;
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                        "Cloning and characterization
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Sikorski R.S., Boguski M.S., Goebl M., Hieter P.A.;
"A repeating amino acid motif in CDC23 defines a family
"A repeating amino acid motif in concentrations are family
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STRAIN-S288C;
MEDLINE-92327848; PubMed-1626431;
Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
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Cell 60:307-317(1990)
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Mol. Cell. Biol. 7:3637-3645(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPR REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88065502; PubMed=3316983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN HAS NO OBVIOUS DNA-BINDING DO DIRECTLY WITH DNA BUT WITH DNA-BOUND SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: CONTAINS 10 TPR DOMAINS.
SIMILARITY: TO YEAST GALL AND CCR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN OTHER SYSTEMS AS A GENERAL REPRESSOR
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         l Similarity
16; Conser
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                                 22.9%;
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         16;
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TPR 3.
TPR 3.
TPR 4.
TPR 5.
TPR 6.
TPR 7.
TPR 8.
TPR 10.
TPR 10
Score 81; DB:
Pred. No. 0.35
16; Mismatches
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         18;
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                                                         Length 966;
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RESULT
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Best Local
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seed storage protein; Signal.
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Belanger F.C., Kriz A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990
15-JUL-1999
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01-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of embryo globulins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89374022; PubMed=2775172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 87-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Physiol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular characterization of the major maize embryo globulin encoded
by the Glbl gene ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHEM. Genet. 27:239-251(1989).

PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS, RESPECTIVELY
                                                                       EEKQ
                                                                                                                     EEKQ 62
                                                                                                                                                                                                                 CRRRCEQQEPRQQYQCQRRCRE-----QQRQHGRGGDLINPQRGGSG-----RYEEG 58
                                                                                                                                                                   CVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADD-----RSGEGSSEDEREREQEK 94
                                                                                                                                                                                                                                                                                           Similarity
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ol. 91:636-643(1989).
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(Rel. 38, Last annotation update)
S ALLELE PRECURSOR (GLB1-S) (7S-LIKE).
                                                                                                                                                                                                                                                                       Conservative
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87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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No.
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                                                                                                                                                                                                                                                                                                                Length 573;
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GLH1_CAEEL

ID GLH1_CAEEL

AC 934689
DT 01-FEB
DT 01-OCT
DE ATP-DE
GN GLH-1.
OS Caenor
OC Enkary
OC Rhabdi
RN [1]
RP SEQUEN
RX MEDLIN
RX PIR; A
DR MITERP
DR INTERP
DR INTERP
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DR MINTS
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TREPEAI
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Best Local
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GLH1_CAEEL SI....

P34689; Q9TXH4;

01-FEB-1994 (Rel. 28, Created)

01-CCT-2000 (Rel. 40, Last sequence update)

01-CCT-2000 (Rel. 40, Last annotation update)

01-CCT-2000 (Rel. 40, Last annotation update)

75 PPENDENT RNA HELICASE GLH-1 (GERMLINE HELICASE-1).
                                                                                                                                    NP_BIND
SITE
SEQUENCE
                                                                                                                                                                             ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                             PFAM; PF00098; zr.c..., PF00098; zr.c..., PF1NTS; PR00939; C2HCZNFINGER.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
Helicase; ATP-binding; RNA-binding; Zinc-finger; Repeat.
Helicase; ATP-binding; RNA-binding; Zinc-finger; Repeat.
7 x 10 AA TANDEM REPEATS, GLY-RICH.
                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roussell D.L., McCrone J.S., Smith P.A., Gruidl M.E., Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: PROBABLE ATP-BINDING RNA HELICASE.
-!- DEVELOPMENTAL STAGE: DURING GERM-LINE PROLIFERATION
-!- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L19948; AAC27384.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "glh-1, a germ-line putative RNA helicase from Caenorhabditis,
four zinc fingers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roussell D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94022363; PubMed=8415696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabdiťidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO;
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 164
                                                                        Local Similarity
                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A48686; A48686.
QQPGHRS-SDCPEPRKEREPRVCYNCQQPGHTSRECTEERKPREGRTGGFGGGAGFGNNG 222
                          RDPQQREYEDCRRRCEQQEPRQQYQCQ----RRCREQQRQH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P05888; 1AAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 90:9300-9304(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000629; -. IPR001410; -. IPR001650; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001878; -.
                                                            Conservative
                                                                                                                                                                  Peloderinae;
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79792
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                                                                        21.0%;
28.6%;
                                                                                                                                    WW;
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                                                          10;
                                                                                                                                                              C2HC-TYPE.
C2HC-TYPE.
C2HC-TYPE.
C2HC-TYPE.
ATP (BY SIMILARITY)).
                                                                        Score 74;
Pred. No.
                                                                                                                                                    DEAD
                                                                                                                                                                                                                                             GLY-RICH.
                                                                                                                                    ADB69DE286A028D6 CRC64;
                                                        Mismatches
                                                                                                                                                    BOX
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1.5;
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                            GRGGDL
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"nit-4, a pathway-specific regulatory gene of Neurospora crassa,
encodes a protein with a putative binuclear zinc DNA-binding
                                                                            DOMAIN
                                                                                                                                                                                                                DNA_BIND
                                                                                                                                                                                                                                   Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yuan G.-F., Marzluf G.A.;
"Molecular characterization of mutations of nit-4, the pathway-specific regulatory gene which controls nitrate
                                                                                                      DOMAIN
                                                                                                                                                                                                                                                            Franscription
                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPRO01138; -.
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01-NOV-1997 (Rel. 35, Last annotation update)
NITROGEN ASSIMILATION TRANSCRIPTION FACTOR NIT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NITRATE AND NITRITE REDUCTASES. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Microbiol. 6:67-73(1992).
FUNCTION: PATHWAY-SPECIFIC REGULATORY GENE OF ASSIMILATION; IT ACTIVATES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLUSTER DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                       P07272; 1PYI
                                                                                                                                                                                                                                                                               PS00463; ZN2_CY6_FUNGAL_1; 1.
PS50048; ZN2_CY6_FUNGAL_2; 1.
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. MW; ~ Y
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881D89172EDD6114 CRC64;
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01-JAN-1990
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Casey R., Domoney C., Stanley J.;
"Convicilin mRNA from pea (Pisum sativum L.) has sequence homology
with other legume 7S storage protein mRNA species.";
Biochem. J. 224:661-666(1984).
-i- FUNCTION: SEED STORAGE PROTEIN.
                                                                                                                                                                                                                                                     EMBL; M73805; AAA33660.1; -.
EMBL; X01379; CAB38247.1; -.
PIR; S02281; S02281.
HSSP; P02853; 2PHL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of a gene in the seeds of transgenic tobacco. Planta 180:461-470(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-296 FROM N.A. Newbigin E.J., Delumen B.O., Chandler P.M., Gould A., Newbigin E.J., Delumen B.O., Chandler P.M., Gould A., Blagrove R.J., March J.F., Kortt A.A., Higgins T.J.; "Pea convicilin: structure and primary sequence of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Pisum.
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INTERPRO; IPR001113; -.
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                                                                                                                                                                                                              storage protein; Multigene family; Signal.
GRYEEGEEK
                           QEDEEEKQKYRYQREKEDEEEKQKYQYQREKKEQKEVQPGRERWEREEDEEQVDEEWRGS
                                                      KRDPQQREYEDCRRRCEQQEPRQQYQCQRRCREQQR-QHGR-----GGDLINPQRGGS 52
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34, Last annotation
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Pred. No. 0.99
17; Mismatches
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ANDR_HUMAN
P10275;
01-MAR-1989
  androgen
Science 2
                                             SEQUENCE OF 189-919 FROM N.A. MEDLINE=88178111; PubMed=3353726;
                                                                                                                                                                                                                                                                                                     MEDLINE=89017168; PubMed=3174628; Chang C., Kokontis J., Liao S.; "Structural analysis of complementary DNA and amino human and rat androgen receptors."; Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=90083302; PubMed=2594783;
Lubahn D.B., Brown T.R., Simental J.A.,
Wilson E.M., French F.S.;
"Sequence of the intron/exon junctions
 "Molecular cloning of huma androgen receptors."; Science 240:324-326(1988).
                                                                                                identification of mutations that cause termination of the receptor protein at complete androgen resistance.";
                                                                                                                                                                                                                                  MEDLINE~89098909; PubMed=2911578; Tilley W.D., Marcelli M., Wilson "Characterization and expression
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French
                                                                                                                                                                              TISSUE-PROSTATE;
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                                                                                                                                                                                                                                                                                                                                                                                                        binding and trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human androgen receptor gene and identification of in a family with complete androgen insensitivity."; Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-MAR-1989 (Rel. 10, Created)
Ol-APR-1990 (Rel. 14, Last sequence update)
Ol-CCT-2000 (Rel. 40, Last annotation update)
ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR)
                                                                                                                                         McPhaul M.J.;
                                                                                                                                                    Marcelli M., Tilley
                                                                                                                                                                MEDLINE=91155943;
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Lubahn D.B., Joseph D.R., Sar M.,
                                                                                                                                "Definition of the
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                  cific region in hormone binding doing and trans-activation by human Endocrinol. 4:417-427(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human androgen receptor: complementary
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                                                                               androgen resistance.";
ocrinol. 4:1105-1116(1990).
                                    Kokontis
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                        J., Liao
of human
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                       rat complementary DNA encoding
                                                                                                                                                                                                                                   J.D.,
of a
                                                                                                                                                    C.M., Griffin J.E.,
                                                                                                                 receptor gene, structure permits the cause androgen resistance: premature
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                                                                "Androgen resistance associated with a receptor at amino acid 772 (Arg-->Cys) decreased messenger ribonucleic acid le receptor function.";
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"A mutation in the ligand binding human LNCaP cells affects steroid
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MEDLINE=91186983; Pub
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Berrevoets C., Claassen E., v
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Nucleic Acids
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Submitted (FEB-1995)
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MEDLINE=88240407: PubMed=3377788;
Trapman J., Klaassen P., Kuiper G.G.J.M.,
Faber P.W., van Rooij H.C.J., Geurts van F
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Wilson E.M.,
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MEDLINE=94108430; PubMed=8281140;
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Lobaccaro J.-M., Lumbroso S., Ktari R., Dumas R., Sulta Pan exonic point mutation creates a MaeIII site in the receptor gene of a family with complete androgen insens
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Newmark J.R., Hardy D.O., Tonb D.C., C
Isaacs W.B., Brown T.R., Barrack E.R.;
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Nakao R., Haji M., Yanase T., Ogo
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Proc. Natl. Acad. Sci. U.S.A. 89:6319-6323(1992).
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Hunt S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
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                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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"A mouse repeat sequence conserved in eukaryotic
J. Submicrosc. Cytol. Pathol. 24:467-472(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                  CAA89800.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Srst.
                                                                                                                                                                                                                                                                                                                                                                                                 35, Created)
35, Last sequence update)
35, Last annotation update)
KDA PROTEIN IN HLJ1-SMP2 IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159
22805 MW;
                                                                                                                                                                                                                                                                                                                      Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72.5; DB Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                       Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) X 8 AA APPROXIMATE TANDEM 8995BEC4EC383971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                 There are no restrictions
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                                                                          http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                 INTERGENIC
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                                                                                                                                                                                                                                                                                                                                       Saccharomycetales
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Hypothetical

protein

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RESULT 11
TRHY_HUMAN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1731-1898 FROM N.A., AND CHARACTERIZATION.
MEDLINE=93315897; PubMed=7686953;
O'Keefe E.J., Hamilton E.H., Lee S.-C., Steinert P.M.;
"Trichohyalin: a structural protein of hair, tongue, nail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRHY_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Invest. Dermatol. 101:65S-71S(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           envelope precursor, and an intermediate linking) protein.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THH OK INIL THOMO Sapiens (Human).

Morazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steinert P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93280194; PubMed=7685034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRICHOHYALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The structure of human trichohyalin. Potential multiple roles as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee S.-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THH OR TRHY OR THL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KRDPQQREYEDCRRCEQQEPRQQYQCQRRCREQQRQHGRGGD----LINPQ
                                                                                                                                                                                                                               SUBUNIT: MONOMER (PROBABLE).

TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCTIONS TO THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AND THE FILLFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE).

DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF
                                                                                     CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
                           PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARC PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                      WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR
SIMILARITY: CONTAINS 2
                                                                                                                                                                                                 DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND
                                                                             DIFFERENT SPECIES.
                                                                                                                                                                                                                    THE EPIDERMIS
                                                                                                                                                                                                                                                                                                              DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                        LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF B' ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim I.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290
605
653
758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 30, Created)
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    Last sequence update)
    Last annotation update)

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637 II
656 MW;
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EF-HAND CALCIUM-BINDING DOMAINS
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Pred.
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POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L.N., O'Keefe E.J., Parry D.A.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BA05BFC754D9294B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein, a cornified cell
filament-associated (cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA
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                                                           200 ARGININES ARE
                            DEIMIDASE.
S-100
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RESULT 12

CBP_HUMAN STANDARD; Q92793; Q16376; O00147; 15-JUL-1998 (Rel. 36, Created)

PRT;

2442

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                                                                         Matches
                                          Query Match
Best Local
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INTERPRO; IPR001751; -
INTERPRO; IPR002048; -
PEAM; PF01023; S_100; 1.
PFAM; PF00036; efhand; 1.
  1723
                                                                       DOMAIN
CONFLICT
CONFLICT
CONFLICT
CONFLICT
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                                                                                                                               REPEAT
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                                                                                                                                                                                                                                                                                                                                                      CA_BIND
                                                                                                                                                                                                                                                                                                                                                            CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00018; EF_HAND; 1. PROSITE; PS00303; S100_CABP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L09190; AAA65582.1; PIR; A45973; A45973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                         REPEAT
                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             Repeat;
                                         Local
         ERDRKFREEEQLRQGREEQQLRSQ-ESDRKFREEEQLRQEREEQQLRPQQRDGKYRWEE 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                            P02633; 1BOC
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                     Calcium-binding.
                                                                         1013
1043
1073
1103
1133
1133
1250
1752
1794
1857
1880
1898
                                 Conservative
                                                                                                                                                                                                                                                       397
                                                                                                                                                                                                                                                                                                                                                      22
62
                                                                         AA;
                                                                                                                        1880
                                       20.3%;
                                                                         247219
                                                            4-8.
23 AA APPROXIMATE TANDEM REPEATS.
23 Y 26 AA APPROXIMATE TANDEM REPEATS.
4 -> L (IN REF. 2).
9 -> K (IN REF. 2).
9 -> K (IN REF. 2).
19 MW; A74B5947FB62E31D CRC64;
                                 10;
                                Score 71.5; DE Pred. No. 5.9; 10; Mismatches
                                                                                                                                                                                                                                                                                                                                     6 x 13 AA TANDEM REPEATS OF R-R-E-Q-E-E-E-R-R-E-Q-Q-L.
                                                                                                                                                                                                                                                                                                                                                     S-100 LIKE.
SITE I (LOW AFFINITY) (POTENTIAL)
SITE II (HIGH AFFINITY) (POTENTIA
                                                                                                                                                                                                                                                                                                                      1-2 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                             1-3 (APPROXIMATE)
                                                                                                                                                                                       x 28
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                                                                                                                                                                                                                                                                                                                             (APPROXIMATE).
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                                                                                                                                                                                       AA APPROXIMATE TANDEM REPEATS AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                              TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions
                                                DB
                                                                                                                                                                                                                                                                                                                                                    AFFINITY) (POTENTIAL).
                                24;
                                                1;
                                               Length 1898
                                Indels
                                                                                                                                                                                                                                                                             OF R-R-E-Q-Q-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration
                                Gaps
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INTERPRO; IPRO00197; -.
INTERPRO; IPRO00433; -.
INTERPRO; IPR001487; -.
PFAM; PF00569; ZZ; 1.
PFAM; PF00439; bromodomain; 1.
PFAM; PF00439; bromodomain; 1.
PFAM; PF00135; Zf-TAZ; 2.
PRINTS; PR00503; BROMODOMAIN.
PROSITE; PS00633; BROMODOMAIN.
PROSITE; PS00633; BROMODOMAIN.
PROSITE; PS00634; BROMODOMAIN.
PROSITE; PS00614; BROMODOMAIN.
PROSITE; PS00634; BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITINE=96376968; PubMed=8782817; Becher R., Behm F.G., Borrow J., Stanton V.P., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Plorsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.; "The translocation t(8;16)(p11:p13) of acute myeloid leukaemia fust a putative acetyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97385172; PubMed-9238046;
MEDLINE-97385172; PubMed-97385172; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giles R.H., Petrij F., Dauwerse H.G., den Hollander A.I., Lushnikova T., van Ommen G.J.B., Goodman R.H., Deaven L.L., Doggett N.A., Peters D.J.M., Breuning M.H.; "Construction of a 1.2-Mb contig surrounding, and molecular analysis of, the human CREB-binding protein (CBP/CREBBP) gene on chromosome 16p13.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U89355, MIM; 600140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                         Transcription
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15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: DEFECTS IN CBP ARE THE CAUSE OF RUBINSTEIN-TAYBI SYNDROME (RTS), A DISCADER CHARACTERIZED EXEMPLIFIES, BROAD THUMBS, BRAAD BIG TOBY, MENTAL RETARDATION AND A PROPENSITY FOR DEVELOPMENT OF MALIGNANCIES.

SIMILARITY: CONTAINS 1 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; U47741; AAC51770.1;
; U85962; AAC51331.1;
; U89354; AAC51339.1;
; U89355; AAC51340.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Enteropean Bioinformatics Institute. There are no resta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELULAR LOCATION: NUCLEAR.
DISEASE: INVOLVED IN ACUTE LEUKEMIAS BY CHROMOSOMAL TRANSLOCATIONS T(8:16) (P11:P13) INVOLVING CBP AND MOZ, AND T(11:16) (Q23:P13.3) INVOLVING CBP AND MLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MEDIATES CAMP-GENE REGULATION BY BINDING SPECIFICALLY TO PHOSPHORYLATED CREB PROTEIN. ACTING AS A COACTIVATOR, CBP AUGMENTS THE ACTIVITY OF PHOSPHORYLATED CREB TO ACTIVATE TRANSCRIPTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMP-RESPONSIVE GENES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institu
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on regulation; Nuclear protein; translocation.
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                                         Activator; Bromodomain;
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MBL outstation -
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RESULT 13
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Best Local S
Matches 21
                                                                                                                                                                                           "Cloning and sequencing of a Livenovicus and genomic structure. Tymphocyte surface protein: cDNA sequence and genomic structure. Proc. Natl. Acad. Sci. U.S.A. 89:10425-10429(1992).

-i- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN B-CELL ACTIVATION. MAY ALSO BE INVOLVED IN SIGNAL TRANSDUCTION AND GENE REGULA:
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01-JUN-1994 (Rel.
01-OCT-1994 (Rel.
          Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
B-LYMPHOCYTE ANTIGEN PRECURSOR (B-LYMPHOCYTE
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Q02832;
                                  EMBL; M99578;
PIR; A46419; /
                                                                     or send
                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                         TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          Mammalia;
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                           SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (PROBABLE). TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED LYMPHOCYTES, VASCULAR ENDOTHELIUM, AND SYNCYTIOTROPHOBLAST.
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                                                                                                                                                                                                                                                     J.R., Wyzykowski R.J., Huang M., Dutton R.W.;
ng and sequencing of a trophoblast-endothelial-activated
                                                                   d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                       Membrane
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FAE -> NSG (IN REF. 2).
ED -> VV (IN REF. 2).
V -> L (IN REF. 2).
N -> F (IN REF. 2).
T -> P (IN REF. 2).
MW: 42D084619475F3D2 CRC64;
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CREB-BINDING.
BROMODOMAIN.
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CHAIN 479
LIPID 2
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                  PFAM;
PFAM;
                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                 Remington M.P., Hoffman P.M., Ruscetti S.K., Masuda M.;
"Complete nucleotide sequence of a neuropathogenic variant of Friend murine leukemia virus PVC-211.";
Nucleic Acids Res. 20:3249-3249(1992).

-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
-!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-POL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
GAG POLYPROTEIN (CORE POLYPROTEIN) (CONTAINS:
P30 AND P10].
                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                        SEQUENCE
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01-AUG-1992
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                                                                                                                                                                                                              INTERPRO;
                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                       Remington M.P., Hoffman P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92319660; PubMed=1620621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses;
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; S35474; S35474.
ERPRO; IPR000840; -.
'ERPRO; IPR001878; -.
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                                                                                                                                             pF02093; Gag_p30; 1.
pF01140; gag_MA; 1.
pF01141; gag_p12; 1.
pF00098; zf-CCHC; 1.
                                                                                                                                   protein;
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s; Retroid viruse
           Similarity
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                                                                                                                                                                                                   IPR002079; -.
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138
550 AA;
   Conservative
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                                                                                                                                                                                                                                             AAA46476.1; -.
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              19
31
            virus (isolate P
es; Retroviridae;
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   13;
Score 70; DB:
Pred. No. 2.7;
L3; Mismatches
                                                                                                                                 Polyprotein; Nucleoprotein;
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                                                                MATRIX PROTEIN P15.
RNA BINDING PHOSPHOPROTEIN CAPSID PROTEIN P30.
NUCLECCAPSID PROTEIN P10.
MYRISTATE (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
CJCNAC. . .) (POTENTIAL).
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e; Mammalian
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                      DB 1;
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2.4;
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ian type C
                     Length 538;
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                                                                                                  P12.
                                                                                                                                 Myristate;
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-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS A
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFF
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytos (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
                                                                                                                                                                                                                                                                                                                   PFAM; PF00104; hormone_rec; 1.
PFAM; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00521; ANDROGENR.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U94177; AAC73048.1; HSSP; P06536; 1RGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98404153; PubMed=9732460; MEDLINE=98404153; PubMed=9732460; Mil
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                                                                    DOMAIN
                                                                                                                                                                                                                                                      DOMAIN
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INTERPRO; IPRO01103; -.
INTERPRO; IPRO01628; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                 NIAMOC
                                                                                                                                                                                                                                                                        Zinc-finger;
                                                                                                                                                                                                                                                                                              Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pean Bioinformatics Institute. There are no restrictions on non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            painen J.A., Wilson E.M.;
primate androgen receptor: a structural basis
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39, Last sequence update)
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(DIHYDROTESTOSTERONE RECEPTOR).
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Query Match

19.8%;

Score

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DB

Length 911;

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Best Local Similarity 32.8%; Pred. No. 4.3;
Matches 19; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

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Db 57 QQQQQQ--QQQQQQQQQQQQQQGETSPRQQQQQGEDGSPQAHRRGPTGYLVLDEEQQ 112

Search completed: March 1, 2001, 16:16:43

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